

JUL 10 2003
PATENT & TRADEMARK OFFICE

Application No. 09/972,268
Declaration under 37 CFR 1.131

3101-A

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Application No: 09/972,268

Applicants: Peter R. Baum, William C. Fanslow III, Timothy E. Lofton,
Eric A. Sorensen, and Adel Youakim

Filed: October 5, 2001

Title: NECTIN POLYPEPTIDES

TC/Art Unit: 1644

Examiner: Maher M. Haddad

Docket No.: 3101-A

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

DECLARATION UNDER 37 C.F.R. § 1.131

We, Peter R. Baum, William C. Fanslow III, Timothy E. Lofton, Eric A. Sorensen,
and Adel Youakim, the undersigned, hereby declare that:

1. This Declaration is made by the inventors of the above-captioned patent application in order to establish a date of invention in the United States prior to April 1, 2000.

2. Prior to April 1, 2000, a DNA clone that encodes human nectin-3 polypeptide (also called "B7L4" polypeptide) had been isolated and its sequence determined in the United States by inventors named in the subject application, as evidenced by the Exhibits A and B enclosed herewith. The works described in Exhibits A and B were completed in this country prior to April 1, 2000.

3. Exhibit A is a copy of a page from one of the laboratory notebooks of Eric A. Sorensen, written in his handwriting, describing a restriction enzyme digest of an isolated lambda phage clone called "HuB7L4 11-1". All dates on the copy have been redacted.

4. Exhibit B (eight pages) is a copy of a computer printout that is incorporated into one of the laboratory notebooks of Eric A. Sorensen, showing the results of the sequencing of the HuB7LA 11-1 clone insert that was performed at the direction of Eric A. Sorensen. The amino acid sequence shown below the corresponding nucleotide sequences is that of human nectin-3 as presented in SEQ ID NO:2 of the above-captioned application (and is identical to amino acids 8 through 549 of SEQ ID NOs 4 and 6). The first page of Exhibit B indicates the location of a predicted signal sequence cleavage site, and the fourth page of Exhibit B indicates the location of the start of the transmembrane domain. All dates on the copy have been redacted.

5. Therefore, on a date prior to April 1, 2000, the inventors of the above-captioned application had determined the amino acid sequence of a human nectin-3 polypeptide including the extracellular domain of a mature form of human nectin-3.

6. As a person signing below: I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

Peter R. Baum

Peter R. Baum

Date: July 1, 2003

William C. Fanslow III

William C. Fanslow III

Date: June 23, 2003

Timothy E. Lofton

Timothy E. Lofton

Date: 23 JUNE 2003

Eric A. Sorensen

Eric A. Sorensen

Date: June 24, 2003

Adel Yeuakim

Date: June 24, 2003

From Page No. 77

ϕ DNA for HuB7C4: plasmids 11-1 and 13 (from kB 18a/g.)
cut in PEG for the 3 weeks I was on vacation.

Spiral out Washed $\times 7$ 70% EtOH Spd vac'd
out heat. Resuspended in 60 μ l H₂O.



Digest ϕ DNAs by EcoRI (NEB m2, buffer) and λ N.T.I (NEB buffer, btl)

- 1) ϕ DNA 11-1 7 EcoRI
- 2) " " " λ N.T.I
- 3) ϕ DNA 13 7 EcoRI
- 4) " " " N.T.I

4 l ϕ DNA

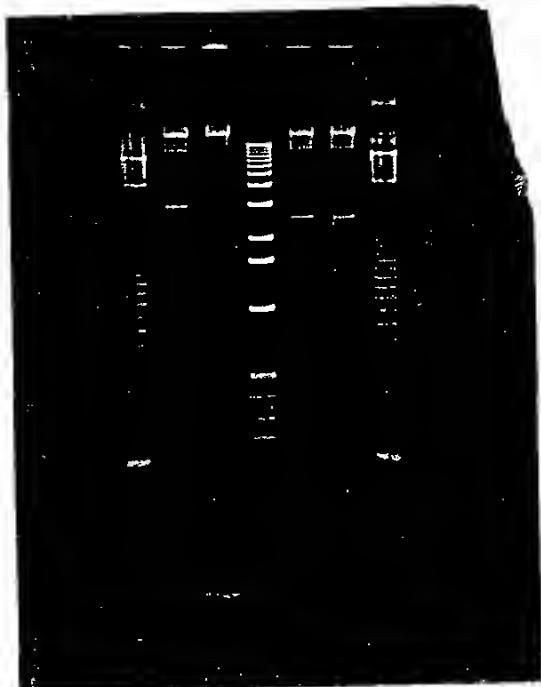
1.5 l λ buffer

5 l enzyme

9 l H₂O
 37°C 60-90'

11-1 @ 95.5 $\mu\text{g}/\text{ml}$

13 @ 57.7 $\mu\text{g}/\text{ml}$



7055 p 80 208

RESULTS:

According to this gel, the clone #13 is way small compared to what I estimated by gelator & Pch I guess I'll see what the DNA sequence is and I'm going to subclone the EcoRI fragment into pBS

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Witnessed & Understood by me,

Barry M. Murphy

Date

Invented by

Recorded by

Date

(Linear) (MinSite=6) MAP of: hub714-11.seq check: 8088 from: 1 to: 3187

HuB7L4 #11 from KB library clone #11-1. Phage DNA: NOT CONFIRMED
sr6527 R. Sorensen
/bertlesj/sorensen/sr6527/hub7l4-11.seq
8139,8140,DPC#9117-20,12233-34,12759-60,12801
HuB7L4-11
With 164 enzymes: *

With 164 enzymes: *



Restriction map diagram showing fragments from EcoRI to BpmI. The fragments are: ApoI (1.0), GdII (0.8), MspAI (0.6), BsiEI (0.4), EaeI (0.3), EagI (0.2), EcoRI (0.1), NotI (0.05), and BpmI (0.0).

34356-->SalI-GCGGGCATGGCCGGACCCCCGGCCC-
 V-D -A G M A R T P G P 34053 →
 CAAAAGAATTGCGGGCGCTGTCCCCGCTGTGTCCTGGAGGC GGCAAAGCACAAC TTCC
 1-----+-----+-----+-----+-----+-----+-----+ 60
 GTTTTCTTAAGCGCCGGCGACAGGGGCGACACAGGACCTCCGCCGTTCTGTTGAAGG
 S P L C P G G G K A O L S

a L L L F P L L L F S R L C G A L A G P I -
 Predicted signal seq. Cleavage ^
 NspI
 AfI III |
 BspLU1II |
 |
 ATTGTGGAGCCACATGTCACAGCAGTATGGGGAAAGAATGTTCAATTAAAGTGTAAATT
 181 -----+-----+-----+-----+-----+-----+ 240

77,85 p. 8

TAACACCTCGGTGTACAGTGTGTCATAACCCCTTCTAACAAAGTAATTTCACAAATTAA
 ← 34054

a I V E P H V T A V W G K N V S L K C L I -

33686 →
 GAAGTAAATGAAACCATAACACAGATTCATGGGAGAAGATAATGGCAAAAGTTCACAG
 241 -----+-----+-----+-----+-----+-----+ 300

a CTTCATTACTTGGTATTGTGTCAAAGTACCCCTTCTATGTACCGTTCAAGTGTC
 E V N E T I T Q I S W E K I H G K S S Q -

XcmI Alol EarI
 | | |
 ACTGTTGCAGTTCACCATCCCCAATATGGATTCTCTGTTCAAGGAGAATATCAGGGAAGA
 301 -----+-----+-----+-----+-----+-----+ 360

TGACAACAGTCAGTGGTAGGGTTATACCTAACAGAGACAAGTTCCCTTATAGTCCTTCT
 ← 33685

a T V A V H H P Q Y G F S V Q G E Y Q G R -

DraI
 |
 GTCTTGTAAATTACTCACTTAATGATGCAACAATTACTCTGCATAACATAGGATTC
 361 -----+-----+-----+-----+-----+-----+ 420

a CAGAACAAATTAAATGAGTGAATTACTACGTTGTTATGAGACGTATTGTATCCTAAG
 V L F K N Y S L N D A T I T L H N I G F -

BmrI
 |
 TCTGATTCTGGAAAATACATCTGCAAAGCTGTTACATTCCCGCTTGGAAATGCCAGTCC
 421 -----+-----+-----+-----+-----+-----+ 480

AGACTAAGACCTTTATGTAGACGTTGACAATGTAAGGGCGAACCTTACGGGTCAAG
 ← 33687

a S D S G K Y I C K A V T F P L G N A Q S -

TCTACAACGTAACTGTGTTAGTGAACCCACTGTGAGCCTGATAAAAGGGCCAGATTCT
 481 -----+-----+-----+-----+-----+-----+ 540

a AGATGTTGACATTGACACAATCAACTGGGTGACACTCGGACTATTTCCCGGTCTAAGA
 S T T V T V L V E P T V S L I K G P D S -

AlwNI 32123 →
 |
 TTAATTGATGGAGGAAATGAAACAGTAGCAGCCATTGCATCGCAGCCACTGGAAAACCC
 541 -----+-----+-----+-----+-----+-----+ 600

a AATTAACCTACCTCCTTACTTGTACCGTGGTAAACGTAGCGTCGGTGACCTTTGGG
 L I D G G N E T V A A I C I A A T G K P -

BmrI
 32121 → |
 GTTGCACATATTGACTGGGAAGGTGATCTTGGTAAATGGAATCCACTACAACCTCTTT
 601 -----+-----+-----+-----+-----+-----+ 660

CAACGTGTATAACTGACCCCTCCACTAGAACCACTTACCTTAGGTGATGTTGAAGAAAA
 ← 33688

a V A H I D W E G D L G E M E S T T T S F -

TatI

|

661 CCAAATGAAACGGCAACGATTATCAGCCAGTACAAGCTATTCCAACCAGATTGCTAGA 720

GGTTTACTTGCCTGCTAATAGTCGGTCATGTTCGATAAAAGGTTGGCTAAACGATCT

a P N E T A T I I S Q Y K L F P T R F A R -

MmeI BssI StyI

| | |

721 GGAAGGCGAATTACTTGTGTTGAAAACATCCAGCCTGGAAAAGGACATCCGATACTCT 780

CCTTCCGCTTAATGAACACAACATTTGTAGGTCGGAACCTTTCTGTAGGCTATGAGA

← 32122

a G R R I T C V V K H P A L E K D I R Y S -

Eco57I

|

781 TTCAATTAGACATACAGTATGCTCCTGAAGTTCGGTACAGGATATGATGGAAATTGG 840

AAGTATAATCTGTATGTCATACGAGGACTTCAAAGCCATTGTCCTATACTACCTTTAAC

a F I L D I Q Y A P E V S V T G Y D G N W -

BsaBI MmeI

| |

841 TTTGTAGGAAGAAAAGGTGTTAATCTCAAATGTAATGCTGATGCAAATCCACCAACCTTC 900

AAACATCCTCTTTCCACAATTAGAGTTACATTACGACTACGTTAGGTGGTGGGAAG

a F V G R K G V N L K C N A D A N P P P F -

Eco57I

BspMI HaeI

| |

901 AAATCTGTGGAGCAGGTTGGATGGACAATGGCCTGATGGTTATTGGCTTCAGACAAT 960

TTTAGACACACCTCGTCCAACCTACCTGTTACCGGACTACCAAATAACCGAAGTCTGTTA

a K S V W S R L D G Q W P D G L L A S D N -

EarI

|

961 ACTCTTCATTTGTCATCCATTGACTTTCAATTATTCTGGTGTATATCTGAAAGTG 1020

TGAGAAGTAAAACAGGTAGGTAACTGAAAGTTAATAAGACCACAAATATAGACATTCAC

a T L H F V H P L T F N Y S G V Y I C K V -

StyI DrdI BstYI Eco57I

| | |

1021 ACCAATTCCCTGGTCAAAGAAGTGCACAAAAAGTCATCTACATTCAGATCCTCCTACT 1080

TGGTTAAGGGAACCAAGTTCTTCACTGGTTTCAGTAGATGTAAGTCTAGGAGGATGA

a T N S L G Q R S D Q K V I Y I S D P P T -

BstYI

ACTACCACCCCTTCAGCCTACAATTCACTGGCATCCCTCAACTGCTGACATCGAGGATCTA
1081 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1140
a T T T L Q P T I Q W H P S T A D I E D L -

HincII

GCAACAGAACCTAAAAAATTGCCCTTCCCATTGTCAACTTTGGCAACAATTAAGGATGAC
1141 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1200
a CGTTGTCTTGGATTTTAACGGGAAGGGTAACAGTTGAAACCGTTGTTAATTCCCTACTG
a A T E P K K L P F P L S T L A T I K D D -

ScaI

MunI	TaqII	BanII	TatI
	BsrDI (Bgl2)	Bsp1286I	EarI

ACAATTGCCACGATCATTGCTAGTGTAGTGGGTGGGCTCTCTTCATAGTACTTGTAAGT
1201 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1260
a TGTTAACGGTGCTAGTAACGATCACATACCCACCCCGAGAGAAGTATCATGAACATTCA
a TGTTAACGGTGC-TCTAGA ← 32124

Start Transmembrane ^ <--34357

a T I A T I I A S V V G G A L F I V L V S -

Bsp24I

SspI	SfcI	BbsI	Bsp24I

GTTCGGCTGGAATATTCTGCTATAGGAGAACGGACGTTCTGGAGACTACTTGCC
1261 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1320
a CAAACCGACCTTATAAGACGATATCCTCTGCCTGCAAAGCACCTCTGATGAAACGG
a V L A G I F C Y R R R R T F R G D Y F A -

AAGAACTACATTCCACCATCAGATATGCAAAAAGAACATCACAAATAGATGTTCTCAACAA
1321 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1380
a TTCTTGATGTAAGGTGGTAGTCTACGTTCTAGTGTATCTACAAGAAGTTGTT
a ← 32125 ♡

K N Y I P P S D M Q K E S Q I D V L Q Q -

GATGAGCTTGTATTCTTACCCAGACAGTGTAAAAAGAAAACAAAATCCAGTGAACAAAT
1381 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1440
a CTACTCGAACTAAGAACATGGGTCTGTCACATTTCTTTGTTTTAGTCACCTGTTA
a D E L D S Y P D S V K K E N K N P V N N -

BsaaI EarI

SnaBI	SapI

CTAATACGTAAAGACTATTTAGAAGAGCCTGAAAAACTCAGTGGAACATGTAGAAAAT
1441 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1500
a GATTATGCATTTCTGATAAAATCTTCTCGGACTTTTTGAGTCACCTGTTACATCTTTA
a L I R K D Y L E E P E K T Q W N N V E N -

BglII
 BstYI
 |
 1501 CTCATAGTTGAAAGACCAATGGATTATTATGAAGATCTAAAATGGATGAAGTTT
 GAGTTATCCAAACTTCTGGTTACCTAATAACTTCTAGATTTTACCCCTACTTC
 a L N R F E R P M D Y Y E D L K M G M K F -
 1560

MsI
 NspI
 AflIII ||
 MsI ||| BspLU1II ||| DrdII
 | | | |
 1561 GTCAGTGATGAAACATTATGATGAAAACGAAGATGACTTAGTTCACATGTAGATGGTTCC
 CAGTCACTACTTGTAATACTACTTTGCTTCTACTGAATCAAAGTGTACATCTACCAAGG
 a V S D E H Y D E N E D D L V S H V D G S -
 1620

BsrGI
 TatI
 (NotI)
 1621 GTAATTCAGGAGGGAGTGGTATGTTAGCAACCACTGAATGTGACTTAACATGTACA
 CATTAAGGTCCCTCCCTACCATAACAAATCGTTGGTGACTTACACTGAATTGATACTGT
 <-34358 -CGCCGGCG
 a V I S R R E W Y V * <-36018

SpeI BclI SmlI
 | | |
 1681 ATGTTCATTACACTAGTTGATCATTTCAGATTGTTCATACTTTCTTGAGGAAGAAT
 TACAAGTAAGTGTGATCAACTAGTAAAGTCTAACAGTATGAAAAAGAACTCCTCTTA
 1740

HindIII Bce83I HindIII
 | | |
 1741 AAGCTTTTCAAGTTGATTTCAAGCTTACTTTATATTCTAATCTGACAAATGAAAAT
 TTCGAAAAAGTTCAACTAAAGTTGAATGAAAAATATAAGATTAGACTGTTACTTTA
 1800

TatI
 Bce83I
 | |
 1801 GTAAAATCTGAGTTCAGTGTATCTAAGCTGCTTACAATTTTTCAATGCTGTACTAC
 CATTAGACTCAAGTCACATAGATTGACGAAATGTTAAAAAAAGTTACGACATGATG
 1860

ApoI
 DraI | ScaI
 SmlI SwaI | TatI |
 | | | |
 1861 TGTCTCAAGATTTAAATTTAATGCAGAGTACTTATTGGTGTGAGGCACACAGGTAAGA
 1920

ACAGAGTTCTAAATTAAAATTACGTCTCATGAAATAACCACACTCCGTGTCCATTCT

HincII

ApoI

DraI

AGAAATGTCAACATTAAATGTATGACTTACTGGTACAAAAATTAAAAGGGAAC

1921 -----+-----+-----+-----+-----+-----+ 1980
TCTTACAGTTGAATTACATACTGAATGAACCAGTTTAAAAAATTTCCTTGA

Tth111II

Bce83I

SmlI

||

ACCTTGACATTGTGTATTAATGTTACCTAACACTATAATCTCAAGTATGATGTTGTT

1981 -----+-----+-----+-----+-----+-----+ 2040
TGGAACGTAAACACATAATTACAAATGGATTCTGATATTAGAGTTCACTACAAACAA

BtsI

HaeIV

ApoI

Hin4I

||

TAACATATACTCTCAAAATTATCACCCTAACATGACACTGCATCAAATTGACTATAA

2041 -----+-----+-----+-----+-----+-----+ 2100
ATTGTATATGGAGAGTTAAATAGTGGTAGTTACTGTGACGTAGTTAACTGATATT

SspI

SspI

AACTAATTCAAGAAATATTATATATTTAAATATACAAAAAATTAGCCTGATG

2101 -----+-----+-----+-----+-----+-----+ 2160
TTGATTAAGTTCTTATAAAATATATATAAAATTATATGTTTTATAATCGGACTAC

Tth111II

||

GAATGGCTTCCCTTCAACATTATTTCTAAGTTCTATACAAATGAAATCTTACCT

2161 -----+-----+-----+-----+-----+-----+ 2220
CTTACCGAAAGGAAAGTTGTAATAAAAGATTCAAAGATATGTTACTTTAGAAATGGA

MslI

VspI

SfcI

||

CTGCATATTAAATGAGCCTGCCATAATTACTGTAGAGTGGCTTTCAAAGATATTTGTT

2221 -----+-----+-----+-----+-----+-----+ 2280
GACGTATAATTACTCGAACGGTATTAATGACATCTCACCGAAAAGTTCTATAAAACAA

EarI

SapI

||

GCACTAAAATGTGGTAGTAAACTCAGTGAACATGATGTTGAAAGAGCATAATTAGCTG

2281 -----+-----+-----+-----+-----+-----+ 2340
CGTGATTTGACACCATCATTGAGTCACTGTACTACACACCTTCTCGTATTAATCGAC

SspI

BspMI

GTCAATATTTGTCCAAAATACCTGCAAGAGTAATAAAATACATACCTTCAAACATGA

2341 -----+-----+-----+-----+-----+-----+ 2400
CAGTTATAAAAACAGGTTTATGGACGTTCTCATTATTTATGTATGGAAAGTTGTACT

Tth111II
 |
 TAATTATTAGTTTTCTGGAACATGGATTGGTACATTAGCAGTAGCCT
 2401 -----+-----+-----+-----+-----+-----+ 2460
 ATTAATAATCAAAAAAAAAGGAAAGACCTGTACCTAAAACCATGTAATCGTCATCGGA

TATTTAATGCTTATGCTCTAACATACTAATAGAAATGAAAAGACGCAGAGAGACAT
 2461 -----+-----+-----+-----+-----+-----+ 2520
 ATAAAATTACGAAATACAGGATTGTATGATTACTTTACTTCTGCGTCTCTCGTA

SpeI
 ScaI|
 TatI ||| Eco57I SfcI ApoI
 | ||| | | | |
 TTGGAAACTGAAAGTACTAGTTTAGAAATGAGACTTCAGCCAACAATCTATAGAAAG
 2521 -----+-----+-----+-----+-----+-----+ 2580
 AAGCCTTATGACTTCATGATCAAATCTTACTCTGAAAGTCGGTTGTTAGATATCTTC

BsrGI
 TatI
 |
 AATTTTATGGACCACATCTGTTTAGTTATTAATGTTGATGTTGTTCAAATGGGTAAATG
 2581 -----+-----+-----+-----+-----+-----+ 2640
 TTAAAATACCTGGTAGAACAAAATCAATAATTACAACATACAACAGTTACCCATTTAC

ApoI
 |
 TACAGAAAGAAAATTTAGAGTAACTTGGAACTTGGATATAACTAGAAAAACTAGAT
 2641 -----+-----+-----+-----+-----+-----+ 2700
 ATGTCTTCTTTAAAATCTCATTGAAACCTTATATTGATCTTTTGATCTA

BsmI
 |
 TATAGAATTAGTCGGTAACACTTGTAAATGGACATTGGCATTCATCTCCTTTCTCCT
 2701 -----+-----+-----+-----+-----+-----+ 2760
 ATATCTTAATCAGCCATTGTGAACGATTACCTGTAAACGTAAGTAGAGGAAAAGGAGGA

AAGTGTATGTATGTGTTAAGATTCTGTTTACGATTAAACTGGAAACATGAGGTT
 2761 -----+-----+-----+-----+-----+-----+ 2820
 TTCACATACATACACAAAATTCTAAAGACAAAAATGCTAATTGACCTTGACTCCAA

TTTGTTTGTGTTTACATAATTACATATATTCTCTGAATCATTTATCTTTGAG
 2821 -----+-----+-----+-----+-----+-----+ 2880
 AAAACAAAAACAAAAAATGTATTAATGTATATAAGGAAGACTTAGTAAATAGAAAACTC

Tth111II SfcI
 | |
 AAAGAAATGTTACCTAAACTCAAATGTGCTTTGTTGAGGTAATTAAATTGCTTC
 2881 -----+-----+-----+-----+-----+-----+ 2940
 TTTCTTACAATGGATTGAAGTTACACGAAAAACAAACACTCCATTAATTAAACGAAG

TACAGTGGAGGCTTACAAAATTATTGTGACAACATTTGAAGCTGAAAGGATAGTTTT
 2941 -----+-----+-----+-----+-----+-----+-----+-----+ 3000
 ATGTCACCTCCGAATGTTAATAACACTGTTGATAAAACTCGACTTCCATCAAAAA

 CTATTGCTAAGTCATTTGAAAAAGTGACCATTGCCAGTGAAATGAAGTGGAAAGTTAGT
 3001 -----+-----+-----+-----+-----+-----+-----+-----+ 3060
 GATAACGATTCACTAAACTTTTCACTGGTAAACGGTCACTTACTTCACCTCAATCA

 AGGAGAATCATAAATTAAATATATTATTGTAAATAAAAAGGCAAAGTAGTAGGTACTT
 3061 -----+-----+-----+-----+-----+-----+-----+-----+ 3120
 TCCTCTTAGTATTAATTATATAATAAAACAATTATTTCCGTTCATCATCCATGAA

DraI	SspI	MspAI	BspAII	BsiEI	EaeI	EagI	GdiII	NotI	ApoI
									EcoRI
TTTAAACCCCTCCAACCAGCCCTTCTCAATATTCAATCTAAACAGCGGCCGGA									BsiEI
3121 -----+-----+-----+-----+-----+-----+-----+-----+ 3180									EaeI
									EagI
									GdiII
									NotI
									ApI
									EcoRI
									BsiEI
									EaeI
									EagI
									GdiII
									NotI
									ApI
									EcoRI
									BsiEI
									EaeI
									EagI
									GdiII
									NotI
									ApI
									EcoRI
									BsiEI
									EaeI
									EagI
									GdiII
									NotI
									ApI
									EcoRI
									BsiEI
									EaeI
									EagI
									GdiII
									NotI
									ApI
									EcoRI
									BsiEI
									EaeI
									EagI
									GdiII
									NotI
									ApI
									EcoRI
									BsiEI
									EaeI
									EagI
									GdiII
									NotI
									ApI
									EcoRI
									BsiEI
									EaeI
									EagI
									GdiII
									NotI
									ApI
									EcoRI